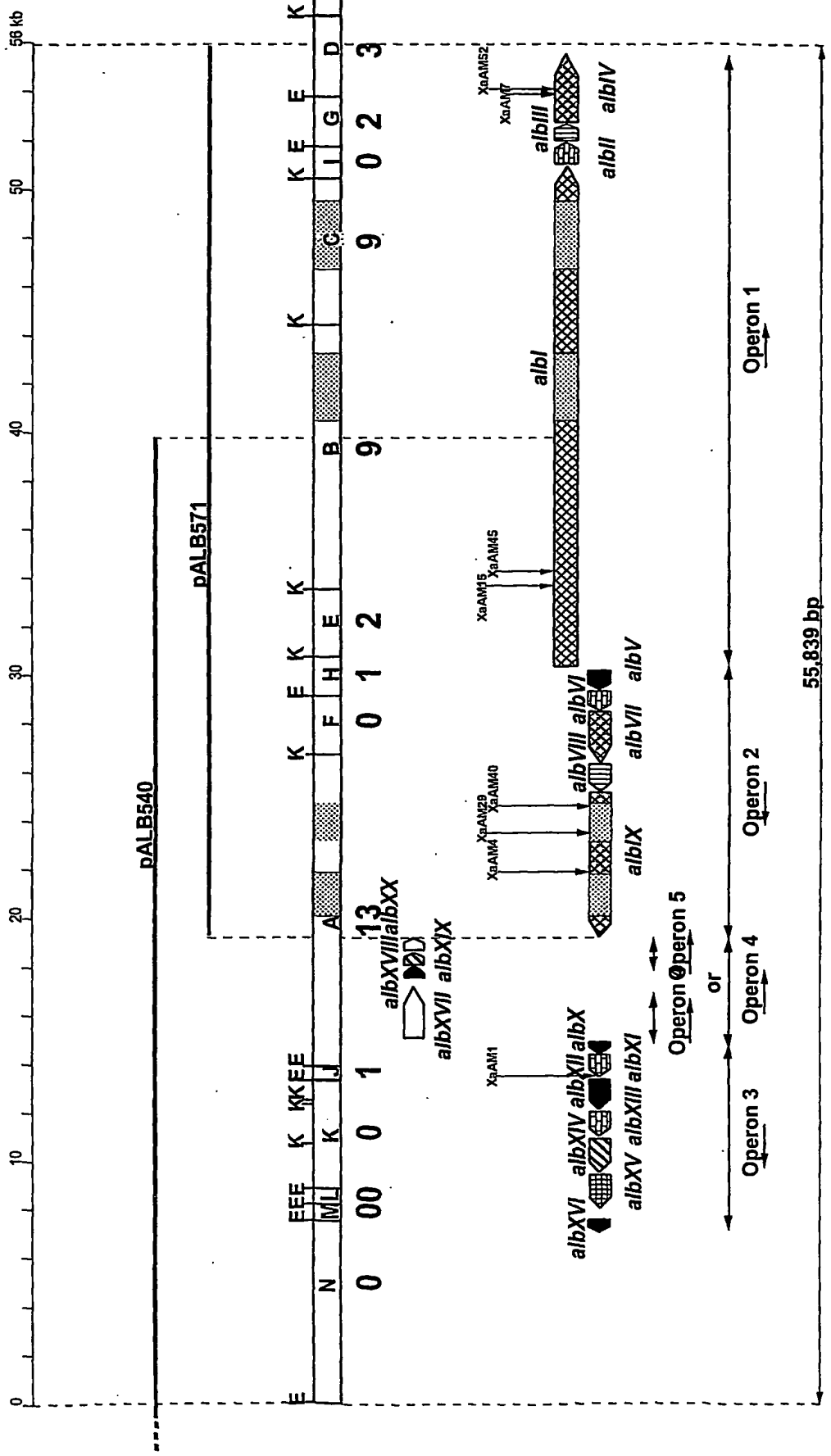

56 kb
50
40
30
20
10
0
pALB571
pALB540
albXVIIIalbXX
albXVII albXIX
albI
albII albIV
albIII
albVIII albVI
albVII albV
albIX
albXVI albXIV albXII albX
albXV albXIII albXI
XbAM1
XbAM4
XbAM29
XbAM40
XbAM15
XbAM45
XbAM52
XbAM7
Operon 1
Operon 2
Operon 3
Operon 4
Operon 5
or
55,839 bp

FIG. 1

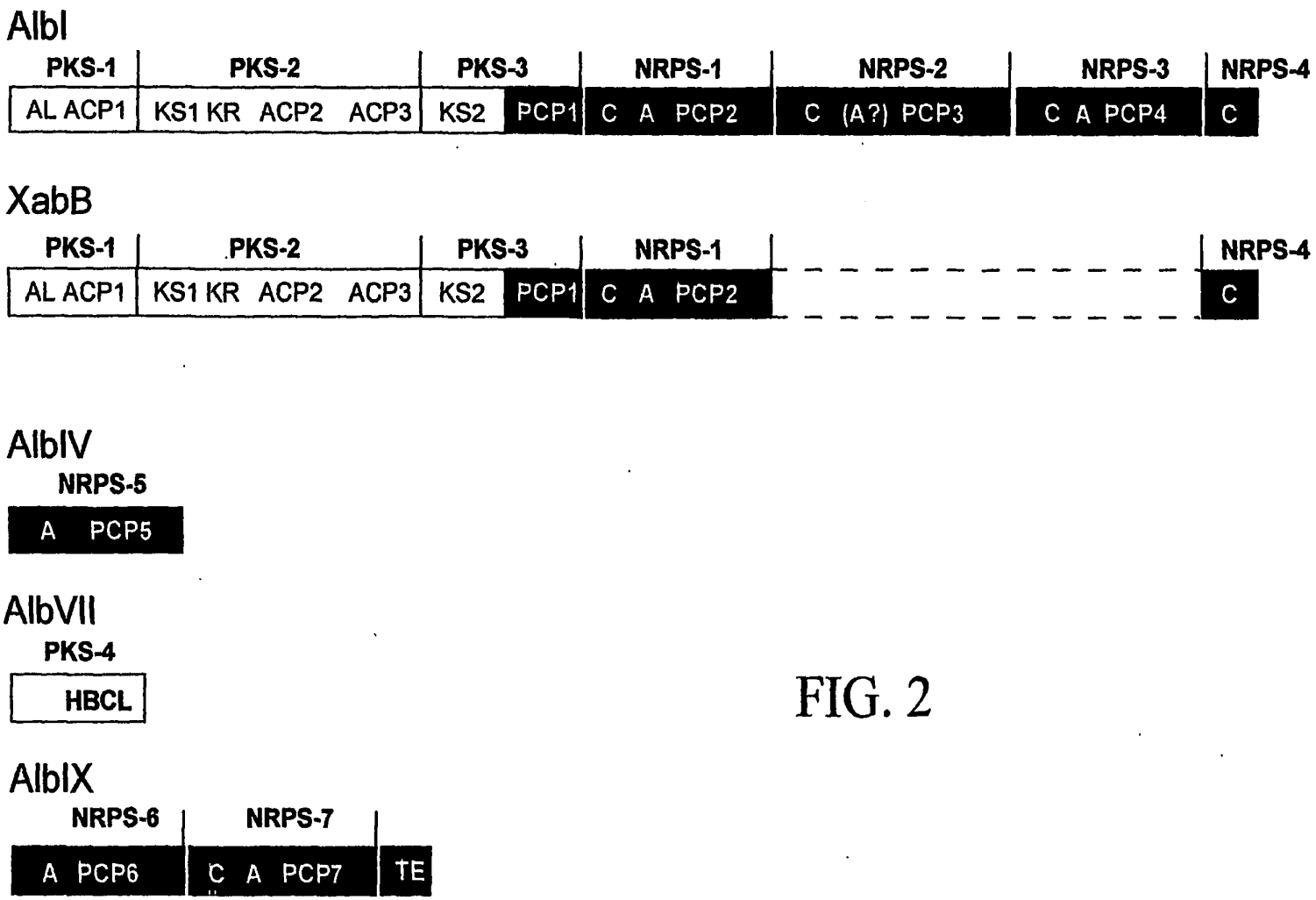

AlbI
PKS-1
PKS-2
PKS-3
NRPS-1
NRPS-2
NRPS-3
NRPS-4
AL ACP1
KS1 KR ACP2 ACP3
KS2
PCP1
C A PCP2
C (A?) PCP3
C A PCP4
C
XabB
PKS-1
PKS-2
PKS-3
NRPS-1
NRPS-4
AL ACP1
KS1 KR ACP2 ACP3
KS2
PCP1
C A PCP2
C
AlbIV
NRPS-5
A PCP5
AlbVII
PKS-4
HBCL
AlbIX
NRPS-6
NRPS-7
A PCP6
C A PCP7
TE

FIG. 2

Sgl-TcmO	173	FVDLGGARG	234	PRADVFIV	263	ALTPGGAVLV
Sgl-TcmN	331	IADLGGGDG	393	TGYDAYLF	423	IGDDDARLLI
Smy-MdmC	64	VLEIGTFTG	135	GAFDIVFV	159	LVRPGGLVAI
Mxa-SafC	63	TLEVGVFTG	134	GTFDLAFI	158	LVRPGGLIIL
Ser-EryG	85	VLDVGFGLG	149	ETFDRVTS	178	VLKPGGVLAI
Spe-DauK	183	VLDVGGGKG	254	RKADAIIL	273	ALEPGGRILI
Sal-DmpM	208	VVDIGGADG	269	GGGDLYVL	298	AMPAHARLLV
Shy-RapM	106	VLEVGCGMG	155	VQGDAEEL	194	ALRRGGALSH
Sav-AveD	71	VLDVGCGSG	124	GSFDAAWA	151	VLRPGGRLAV
Sar-Cmet	158	VLDVACGHG	220	GPYDLSLI	251	ATRPGGRIGI
AlbII	174	VLDVAAGHG	236	SGYDVILL	267	ALNDDGMVIT
		Motif I		Motif II		Motif III

FIG. 3

Sgl-tcmP	84	VVLHLACGLDSRAFRMDVPD	109	DVDVPDVIELR	139	EDWLDTVP	150	PALVVAEGLTPYL
Sme-PKS	84	TVLHLGCGLDSRIFRIDPGP	109	ELDVPDVISLR	139	RGWIERLP	150	PTMIVAEGVLPYL
Pmu-tcmP	86	VVVQLGAGLDARFERLGKPQ	111	DLDLPEVINIR	141	TDWMKTVS	152	PVLLILEGVLMFF
Mtu-Omt	85	TVVALAEGLQTSFWRLDVAI	113	TVDLPPIVDLR	144	YSWMDSVD	155	GVFITAEGLLMYL
Mlo-Hp	84	IVLHLGCGLDTRVFRVDPPP	109	DADYPQVIELR	139	PGWLAEVP	150	PAMVVAEGLTPYL
Mtu-Hp	101	QVAILASGLDSRAYRLPWPT	127	EIDQPKVMEFK	162	ADWPTALQ	178	PTAWLAEGLLIYL
Mtu-Hp2	104	QVVILASGDLSRAWRLPWPD	129	ELDQPKVLEFK	162	QDWPKALQ	178	PCAWLAEGLVRYL
Mtu-Hp3	98	QVVILAAGLDSRAYRLPWPD	123	ELDRPQVLDFK	156	DDWPQALR	172	PSAWIAEGLLIYL
Mtu-Hp4	101	QAVIVAAGLDCRAYRLDWQP	126	EIDVPKVLEFK	161	TDWPTPLT	177	PSAWSVEGLLPYL
Sco-Hp	93	QVVLLGAGMDSRAFRMAWPE	118	EVDTPAPLEFK	153	EDWPSALA	169	PTAWIGEGLLIYL
AlbVI	99	QVVILAAGMDARAYRLPWPS	124	EIDHMDVLSDK	157	EDWPQALK	173	ATLWLVEGLLCYL
	Motif I		Motif II		Motif III		Motif IV		

FIG. 4

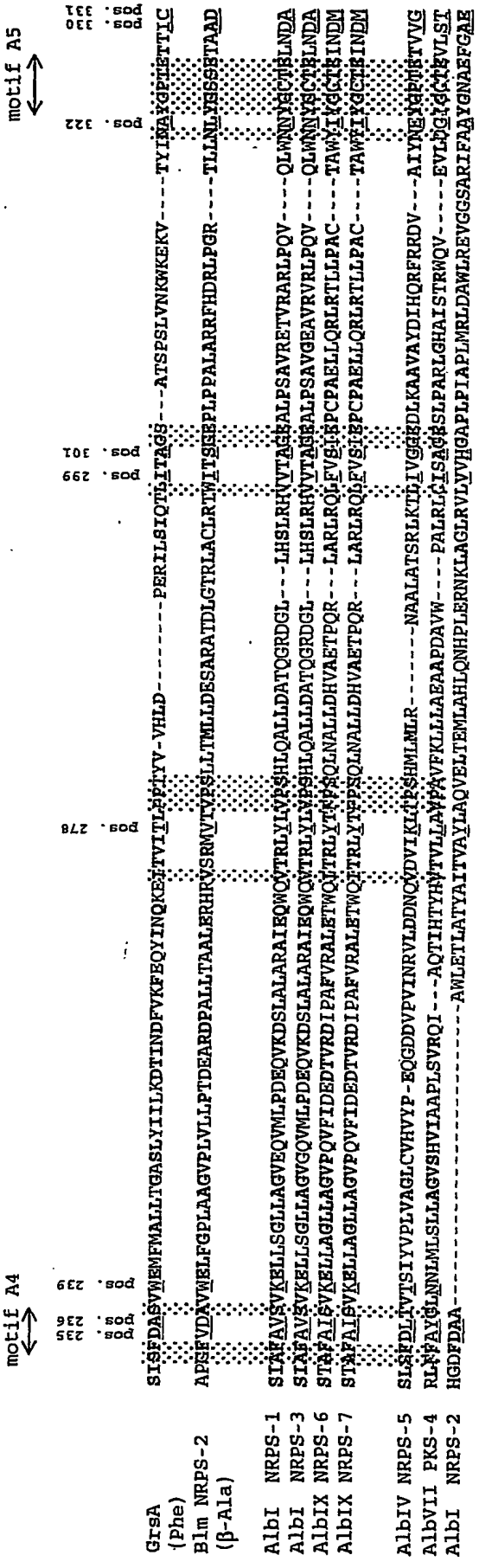
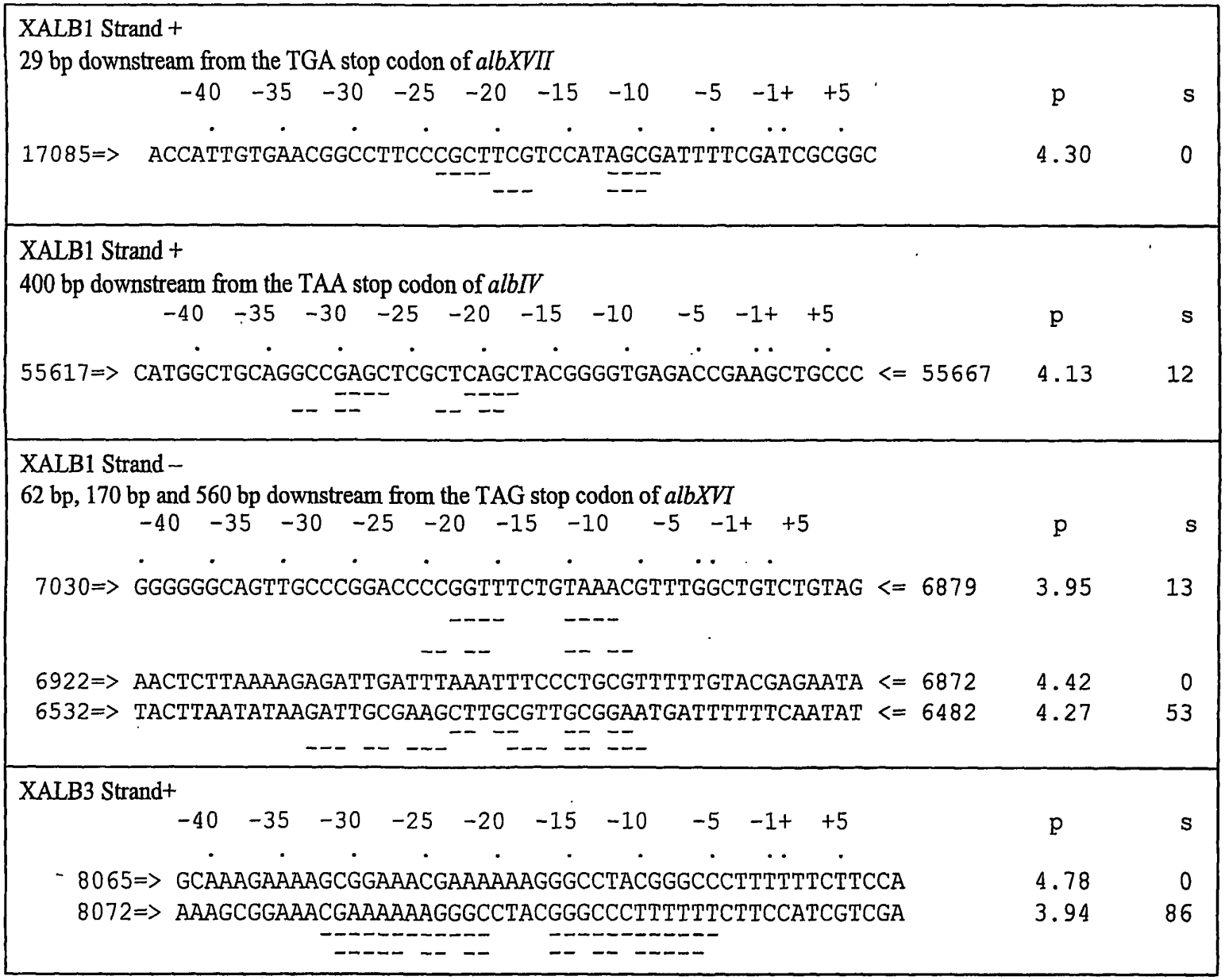

motif A4
motif A5
pos. 239
pos. 236
pos. 235
pos. 278
pos. 299
pos. 301
pos. 322
pos. 330
pos. 331
GrsA (Phe)
Blm NRPS-2 (β-Ala)
AlbI NRPS-1
AlbI NRPS-3
AlbIX NRPS-6
AlbIX NRPS-7
AlbIV NRPS-5
AlbVII PKS-4
AlbI NRPS-2

FIG. 5

FIG. 6


XALB1 Strand +
29 bp downstream from the TGA stop codon of albXVII
-40 -35 -30 -25 -20 -15 -10 -5 -1+ +5
p
s
17085=> ACCATTGTGAACGGCCTTCCCGCTTCGTCCATAGCGATTTTCGATCGCGGC
4.30
0
XALB1 Strand +
400 bp downstream from the TAA stop codon of albIV
-40 -35 -30 -25 -20 -15 -10 -5 -1+ +5
p
s
55617=> CATGGCTGCAGGCCGAGCTCGCTCAGCTACGGGGTGAGACCGAAGCTGCCC <= 55667
4.13
12
XALB1 Strand –
62 bp, 170 bp and 560 bp downstream from the TAG stop codon of albXVI
-40 -35 -30 -25 -20 -15 -10 -5 -1+ +5
p
s
7030=> GGGGGGCAGTTGCCCGGACCCCGGTTTCTGTAAACGTTTGGCTGTCTGTAG <= 6879
3.95
13
6922=> AACTCTTAAAAGAGATTGATTTAAATTTCCCTGCGTTTTTGTACGAGAATA <= 6872
4.42
0
6532=> TACTTAATATAAGATTGCGAAGCTTGCGTTGCGGAATGATTTTTTCAATAT <= 6482
4.27
53
XALB3 Strand+
-40 -35 -30 -25 -20 -15 -10 -5 -1+ +5
p
s
8065=> GCAAAGAAAAGCGGAAACGAAAAAAGGGCCTACGGGCCCTTTTTTCTTCCA
4.78
0
8072=> AAAGCGGAAACGAAAAAAGGGCCTACGGGCCCTTTTTTCTTCCATCGTCGA
3.94
86

```
14456 GTCGTTGATCAGCACCAGATAAGCCTGTTCCTCGAACGTCATCCTAAAGATACCCCCGGAAGGCTGCTGCGAAGCACGGAAGTTGCTACATCGCAC
      CAGCAACTAGTCGTGGTCTATTCGGACAAGGAGCTTGCAGTAGGATTTCTATGGGGGCCTTCCGACGACGCTTCGTGCCTTCAACGATGTAGCGTG
       D  N  I  L  V  L  Y  A  Q  E  E  F  T  M          RBS
                  albX
            -35 (PalbX: operon 3)    -10 (PalbX: operon 3)
14552 AATGCGATTCAGATGGACCAAGCAAAGCGACTATACATGACGTCACTTCGAAGATGTCAAGAAAAATAGCGCGTGAAGAGCACGTAAGAGTGATGT
      TTACGCTAAGTCTACCTGGTTCGTTTCGCTGATATGTACTGCAGTGAAGCTTCTACAGTTCTTTTTATCGCGCACTTCTCGTGCATTCTCACTACA
                                  -10 (PalbXVII: operon 4) -35 (PalbXVII: operon4)

14648 GTTTCGCACCGCTGTACGTCCCATCGCCATCGCGGCAAAGCTTACACGAAAAATTCACCAGGGCATGCGTTCAATACGCGGGTCAAAGCAATATCC
      CAAAGCGTGGCGACATGCAGGGTAGCGGTAGCGCCGTTTCGAATGTGCTTTTTAAGTGGTCCCGTACGCAAGTTATGCGCCCAGTTTCGTTATAGG

14744 TTGCGCTTGCAGAGCTATGTTCGTGCGTAAAGCGCCAAGGCAGTGGGGAGCAACACCTTGGGTTTCGGTTGAGGTGCGGGTAGCAATTTCTGCTTA
      AACGCGAACGTCTCGATACAAGCACGCATTTCGCGGTTCCGTCACCCCTCGTTGTGGAACCCAAAGCCAACTCCACGCCCATCGTTAAAGACGAAT

                                                                  RBS
14840 ATATCCACGCGCGGCGGTTTTTGTCTTGCCGGGCGTCAACTGTCTCATCGAGCAGTCTGGGAGGCTATTTTGCGCTGCCTTATCATAAATAATTAC
      TATAGGTGCGCGCCGCCAAAAACAGAACGGCCCGCAGTTGACAGAGTAGCTCGTCAGACCCTCCGATAAAACGCGACGGAATAGTATTTATTAATG
                                                                    M  R  C  L  I  I  N  N  Y
                                                                       albXVII
```

FIG. 7A

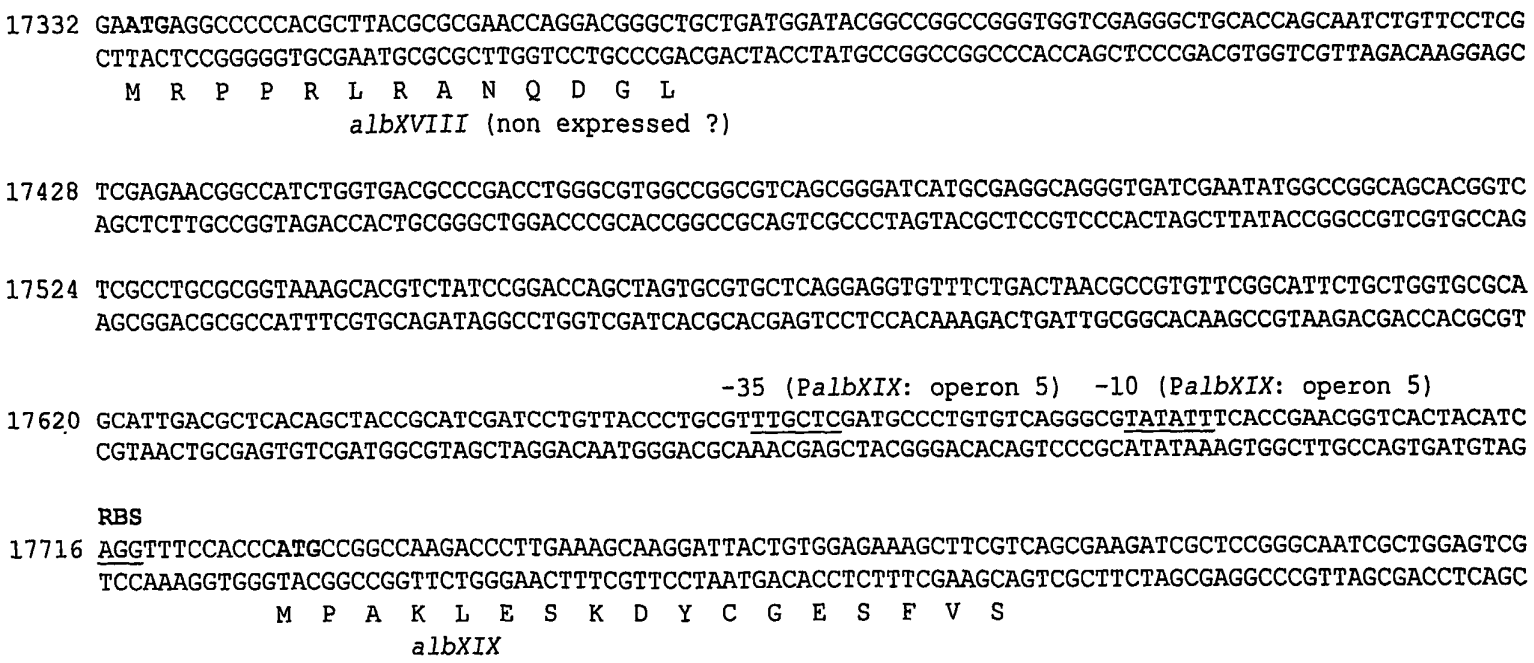

17332 GAATGAGGCCCCCACGCTTACGCGCGAACCAGGACGGGCTGCTGATGGATACGGCCGGCCGGGTGGTCGAGGGCTGCACCAGCAATCTGTTCCTCG
CTTACTCCGGGGGGTGCGAATGCGCGCTTGGTCCTGCCCGACGACTACCTATGCCGGCCGGCCCACCAGCTCCCGACGTGGTCGTTAGACAAGGAGC
M R P P R L R A N Q D G L
albXVIII (non expressed ?)
17428 TCGAGAACGGCCATCTGGTGACGCCCGACCTGGGCGTGGCCGGCGTCAGCGGGATCATGCGAGGCAGGGTGATCGAATATGGCCGGCAGCACGGTC
AGCTCTTGCCGGTAGACCACTGCGGGCTGGACCCGCACCGGCCGCAGTCGCCCTAGTACGCTCCGTCCCACTAGCTTATACCGGCCGTCGTGCCAG
17524 TCGCCTGCGCGGTAAAGCACGTCTATCCGGACCAGCTAGTGCGTGCTCAGGAGGTGTTTCTGACTAACGCCGTGTTCGGCATTCTGCTGGTGCGCA
AGCGGACGCGCCATTTCGTGCAGATAGGCCTGGTCGATCACGCACGAGTCCTCCACAAAGACTGATTGCGGCACAAGCCGTAAGACGACCACGCGT
-35 (PalbXIX: operon 5) -10 (PalbXIX: operon 5)
17620 GCATTGACGCTCACAGCTACCGCATCGATCCTGTTACCCTGCGTTTGCTCGATGCCCTGTGTCAGGGCGTATATTTCACCGAACGGTCACTACATC
CGTAACTGCGAGTGTCGATGGCGTAGCTAGGACAATGGGACGCAAACGAGCTACGGGACACAGTCCCGCATATAAAGTGGCTTGCCAGTGATGTAG
RBS
17716 AGGTTTCCACCCATGCCGGCCAAGACCCTTGAAAGCAAGGATTACTGTGGAGAAAGCTTCGTCAGCGAAGATCGCTCCGGGCAATCGCTGGAGTCG
TCCAAAGGTGGGTACGGCCGGTTCTGGGAACTTTCGTTCCTAATGACACCTCTTTCGAAGCAGTCGCTTCTAGCGAGGCCCGTTAGCGACCTCAGC
M P A K L E S K D Y C G E S F V S
albXIX

FIG. 7B

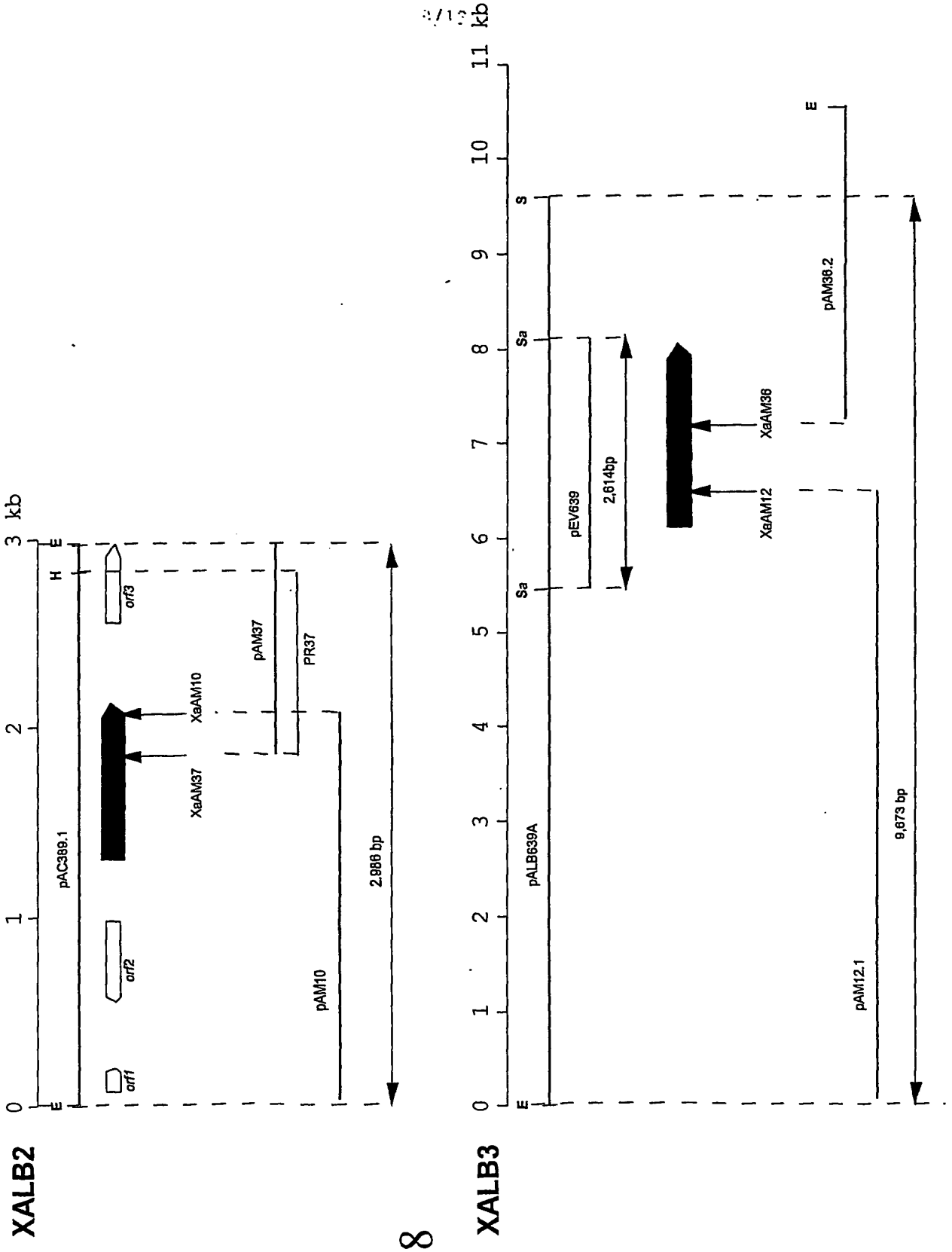

XALB2
3 kb
2
1
0
E
H
E
pAC389.1
orf1
orf2
orf3
XaAM10
XaAM37
pAM37
PR37
pAM10
2,986 bp
XALB3
11 kb
10
9
8
7
6
5
4
3
2
1
0
E
S
Sa
Sa
pALB639A
pEV639
2,614bp
XaAM38
XaAM12
pAM38.2
pAM12.1
9,673 bp

FIG. 8

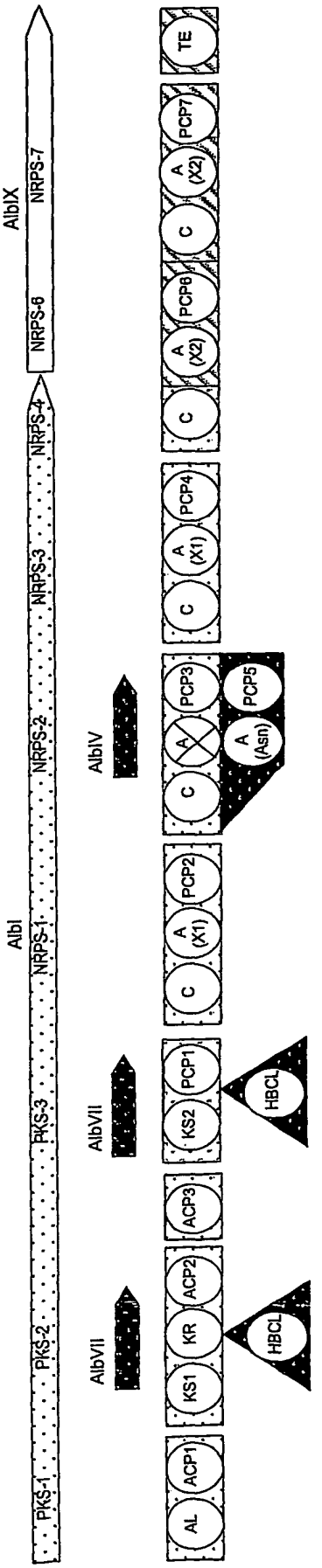

AlbI
AlbIX
PKS-1
PKS-2
PKS-3
NRPS-1
NRPS-2
NRPS-3
NRPS-4
NRPS-6
NRPS-7
AlbVII
AlbVII
AlbIV
AL
ACP1
KS1
KR
ACP2
ACP3
KS2
PCP1
HBCL
C
A (X1)
PCP2
C
A
PCP3
A (Asn)
PCP5
C
A (X1)
PCP4
C
A (X2)
PCP6
C
A (X2)
PCP7
TE

FIG. 9A

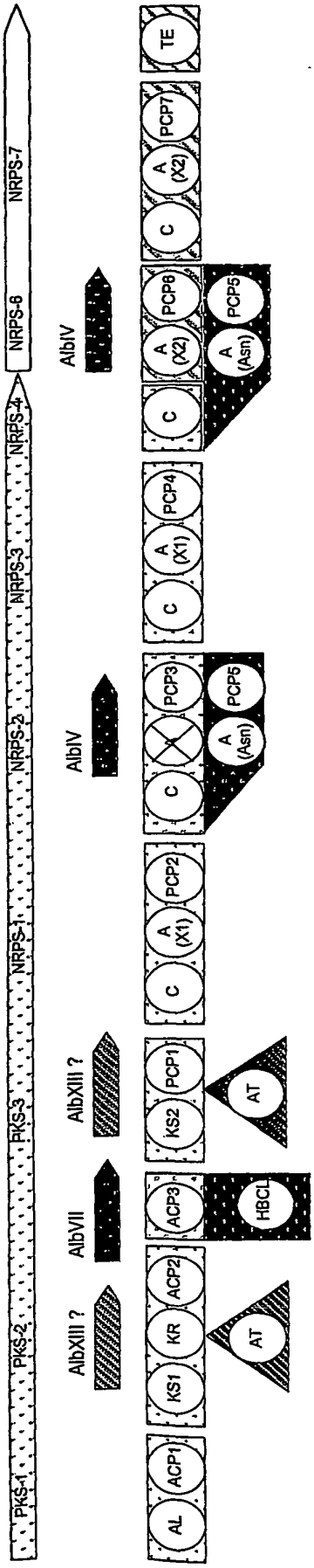

AlbI
AlbIX
PKS-1
PKS-2
PKS-3
NRPS-1
NRPS-2
NRPS-3
NRPS-4
NRPS-6
NRPS-7
AlbXIII ?
AlbVII
AlbXIII ?
AlbIV
AL
ACP1
KS1
KR
ACP2
ACP3
KS2
PCP1
HBCL
AT
C
A (X1)
PCP2
C
A
PCP3
A (Asn)
PCP5
C
A (X1)
PCP4
C
A (X2)
PCP6
C
A (X2)
PCP7
TE

FIG. 9B

RifA-1	LGRVDVLQPAC**FA**VMVG**L**AAVWESV**GV**R**P**DAVV**GHS**Q**GE**I
RifA-2	LDQTMYTQGAL**FA**VETA**L**FRLFESW**GV**R**P**GLLA**GHS**I**GE**L
RifA-3	LDRVDVVQPAS**FA**MMVG**L**AAVWTSL**GV**T**P**DAVL**GHS**Q**GE**I
RifB-1	LDRVDVVQPAS**FA**VMVG**L**AAVWESV**GV**R**P**DAVV**GHS**Q**GE**I
RifE-1	LNQTVFTGAGL**FA**VESA**L**FRLAESW**GV**R**P**DVVL**GHS**I**GE**I
BlmVIII	ADDTRAAQPAL**FA**VEYA**L**ARTLMDW**GV**R**P**AAML**GHS**L**GE**V

FIG. 10A

AlbXIII	LEDRPRHIRAVIDTLTGHAQFGPAIQAHNVAVI**GHS**V**G**GY
FenF	TRTMNAQPAILTVSVIAYQVYMQEI**G**IK**P**HFLA**GHS**L**GE**Y
LipA	PDSRGRQLLAALDYLTGRSSVRGRIDSGRLGVM**GHS**M**G**GG

FIG. 10B

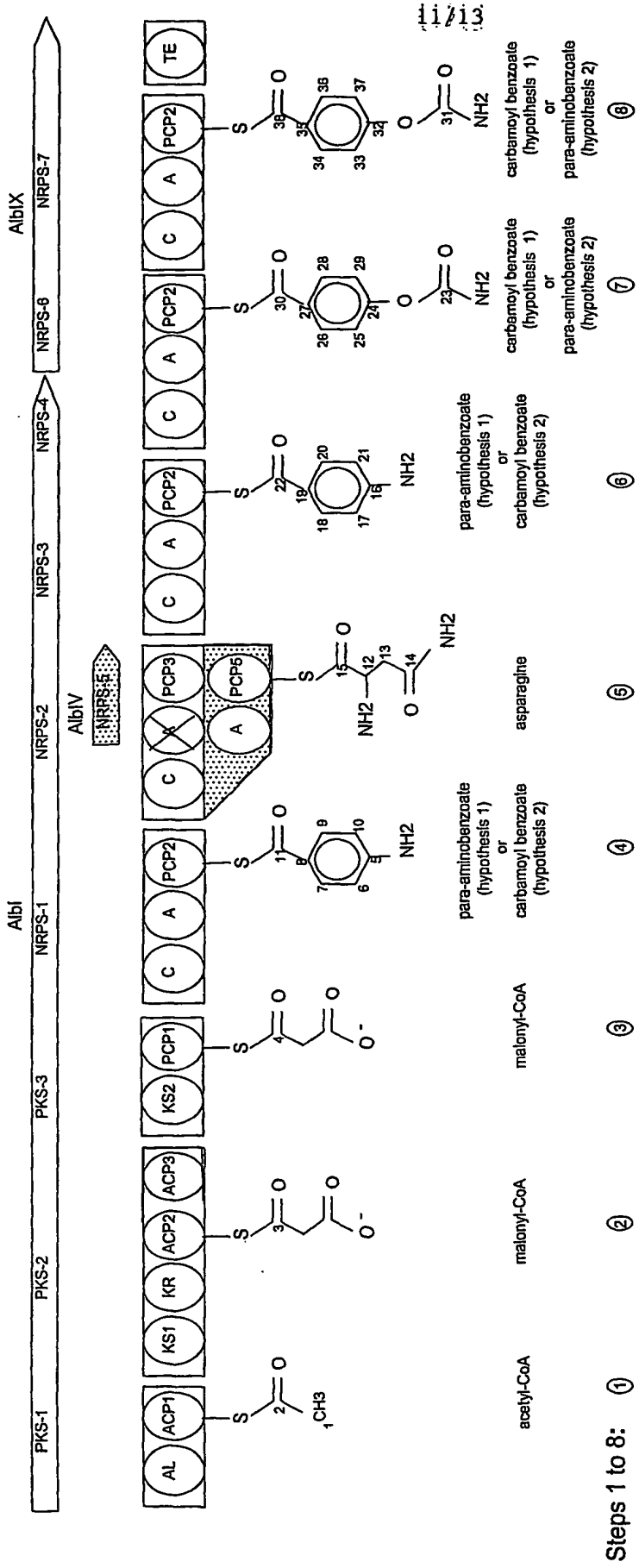
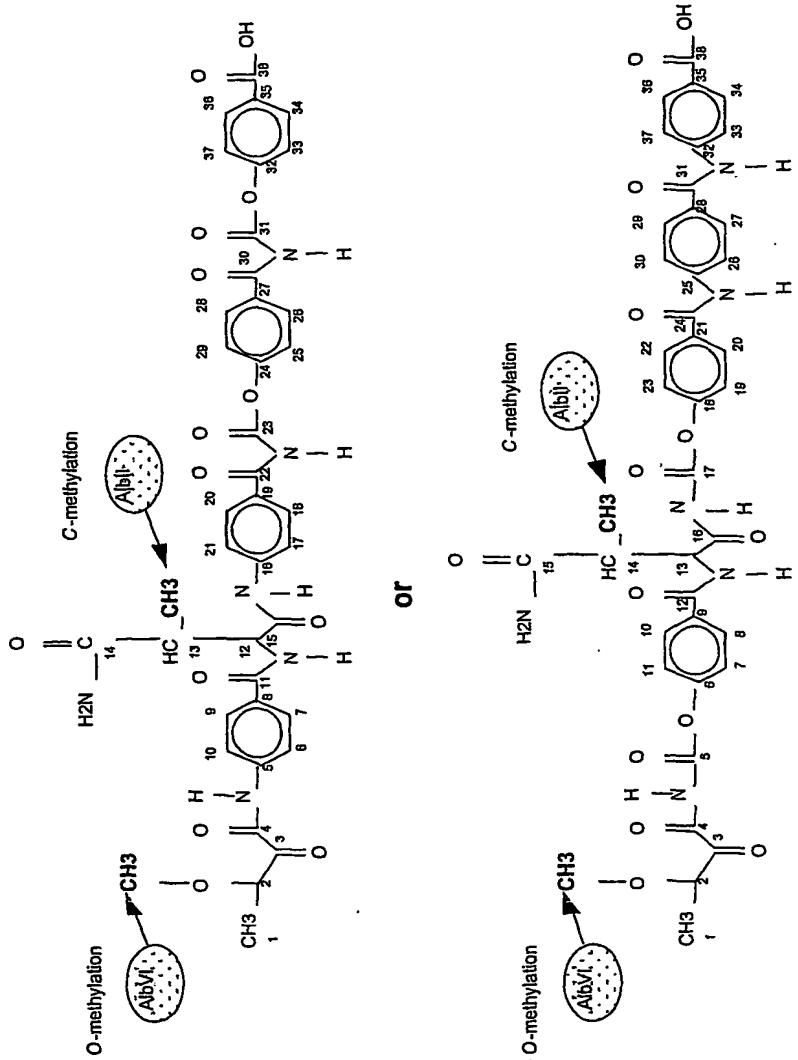

AlbI
AlbIV
AlbIX
PKS-1
PKS-2
PKS-3
NRPS-1
NRPS-2
NRPS-3
NRPS-4
NRPS-6
NRPS-7
NRPS-5
AL
ACP1
KS1
KR
ACP2
ACP3
KS2
PCP1
C
A
PCP2
PCP3
PCP5
TE
acetyl-CoA
malonyl-CoA
malonyl-CoA
para-aminobenzoate (hypothesis 1) or carbamoyl benzoate (hypothesis 2)
asparagine
para-aminobenzoate (hypothesis 1) or carbamoyl benzoate (hypothesis 2)
carbamoyl benzoate (hypothesis 1) or para-aminobenzoate (hypothesis 2)
carbamoyl benzoate (hypothesis 1) or para-aminobenzoate (hypothesis 2)
Steps 1 to 8: ① ② ③ ④ ⑤ ⑥ ⑦ ⑧

FIG. 11A



$C_{40}O_{15}N_6H_{35}$
(molecular weight : 839)

FIG. 11B

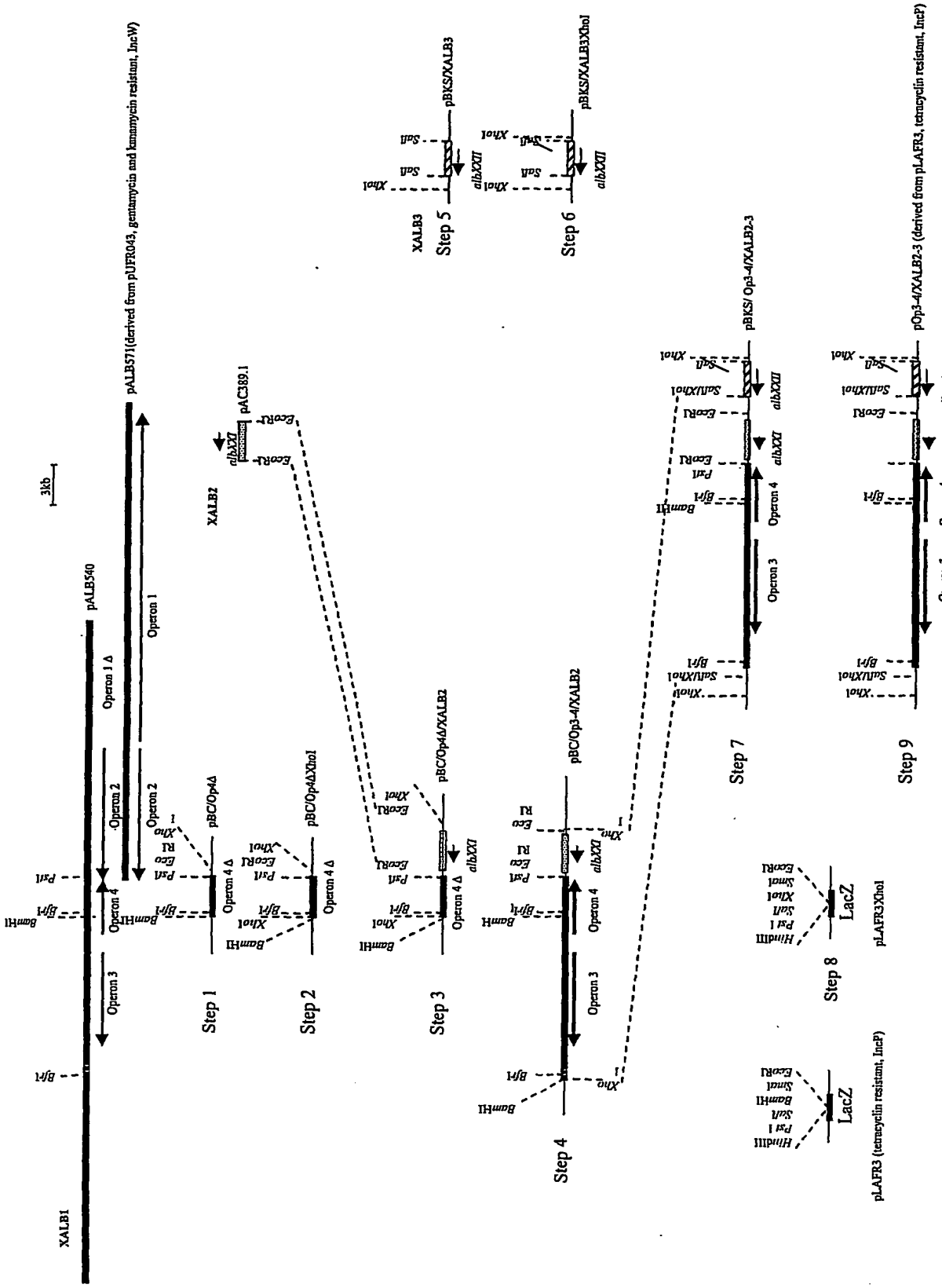

pALB571(derived from pUFR043, gentamycin and kanamycin resistant, IncW)
pALB540
XALB1
XALB2
XALB3
pAC389.1
pBC/Op4Δ
pBC/Op4ΔXhoI
pBC/Op4ΔXALB2
pBCOp3-4/XALB2
pBKS/ Op3-4/XALB2-3
pOp3-4/XALB2-3 (derived from pLAFR3, tetracyclin resistant, IncP)
pBKS/XALB3
pBKS/XALB3XhoI
pLAFR3 (tetracyclin resistant, IncP)
pLAFR3XhoI
Operon 1
Operon 1 Δ
Operon 2
Operon 3
Operon 4
Operon 4 Δ
albXXI
albXXII
albXXIII
LacZ
Step 1
Step 2
Step 3
Step 4
Step 5
Step 6
Step 7
Step 8
Step 9
3kb

FIG. 12